

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/579879A
Source: FFWO
Date Processed by STIC: 3/6/07

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IFWO

RAW SEQUENCE LISTING

DATE: 03/06/2007

PATENT APPLICATION: US/10/579,879A

TIME: 11:32:00

Input Set : N:\efs\03_06_07

\10579879A_efs\Replacement_Sequence_Listing.txt

Output Set: N:\CRF4\03062007\J579879A.raw

3 <110> APPLICANT: The Government of the United States of America, as
 4 represented by the Secretary of the Department of Health and
 5 Human Services
 6 Flomerfelt, Francis
 7 Gress, Ronald
 9 <120> TITLE OF INVENTION: SPATIAL FOR ALTERING CELL PROLIFERATION
 11 <130> FILE REFERENCE: 4239-64851-02
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/579,879A
 14 <141> CURRENT FILING DATE: 2006-05-17
 16 <150> PRIOR APPLICATION NUMBER: PCT/US2003/036874
 17 <151> PRIOR FILING DATE: 2003-11-18
 19 <160> NUMBER OF SEQ ID NOS: 7
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 933
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Mus musculus
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (84)..(677)
 32 <223> OTHER INFORMATION: Coding sequence
 34 <400> SEQUENCE: 1
 35 tcttgagggtt gccaattttt tttttttttt tttttttttt tttttttttt gggttgggga 60
 37 gaaacttggtg ttggaaccag ccc ctg ttt ctg ggg aat gta tat aag ggg agt 113
 38 Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser
 39 1 5 10
 41 tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag 161
 42 Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
 43 15 20 25
 45 cca gag acg aag ccg gag aac ctt cca agg agc cac ggg gat gtt ggg 209
 46 Pro Glu Thr Lys Pro Glu Asn Leu Pro Arg Ser His Gly Asp Val Gly
 47 30 35 40
 49 ctc cag aaa gag act gtg gtc cca ggc att gtg gat ttc gag ctg atc 257
 50 Leu Gln Lys Glu Thr Val Val Pro Gly Ile Val Asp Phe Glu Leu Ile
 51 45 50 55
 53 cat gag gag ctg aag acc aca aag ccc caa aca tca caa cca aca ccc 305
 54 His Glu Glu Leu Lys Thr Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro
 55 60 65 70
 57 agt gcc tac cgc ttt gga cgc cta agc cac cat tcc ttc ttc tcg agg 353
 58 Ser Ala Tyr Arg Phe Gly Arg Leu Ser His His Ser Phe Phe Ser Arg
 59 75 80 85 90
 61 cac cac ccc caa cca cag cga gtg act cat atc caa gat atc gct ggg 401
 62 His His Pro Gln Pro Gln Arg Val Thr His Ile Gln Asp Ile Ala Gly

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63          95          100          105
65 aag cct gtc tgc gtg gtc agg gac gag ttc tct ctg tcg gcc ttg act      449
66 Lys Pro Val Cys Val Val Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr
67          110          115          120
69 cag ccc aca ttc tta tcc cgc tgt ctg atg ggg atg ccc acc atc tct      497
70 Gln Pro Thr Phe Leu Ser Arg Cys Leu Met Gly Met Pro Thr Ile Ser
71          125          130          135
73 gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt tct act      545
74 Val Pro Ile Gly Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr
75          140          145          150
77 tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga gtg act      593
78 Ser Asp Thr Trp Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg Val Thr
79 155          160          165          170
81 gtc ttc act aag gaa atc cag cca aag ccc gat gag gtt ggt gtt gca      641
82 Val Phe Thr Lys Glu Ile Gln Pro Lys Pro Asp Glu Val Gly Val Ala
83          175          180          185
85 caa aga atg gag cct aga aaa aaa agg cct tct taa gtctcccaaa      687
86 Gln Arg Met Glu Pro Arg Lys Lys Arg Pro Ser
87          190          195
89 tgctcagctg ctggcacggg aggggaagga cctcataac ctgcaagggtg acagcgaaaa      747
91 tcaaagaac acaaaatcac acctagcaga gaaatccaag aagggttccc agaaacaccc      807
93 tctaaagcaa ctgttcccaa cctgtctaat gccttgaccc ttgaatacag tttctcacac      867
95 tgcagtaacc cctgcccccg aaataaaatt attttcatta ctacttcaaa aaaaaaaaaa      927
97 aaaaaa      933

100 <210> SEQ ID NO: 2
101 <211> LENGTH: 197
102 <212> TYPE: PRT
103 <213> ORGANISM: Mus musculus
105 <400> SEQUENCE: 2
107 Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser Leu Ala Pro Arg Arg Asp
108 1          5          10          15
111 Glu Val Thr Ser Pro Lys Ala Glu Pro Gln Pro Glu Thr Lys Pro Glu
112          20          25          30
115 Asn Leu Pro Arg Ser His Gly Asp Val Gly Leu Gln Lys Glu Thr Val
116          35          40          45
119 Val Pro Gly Ile Val Asp Phe Glu Leu Ile His Glu Glu Leu Lys Thr
120          50          55          60
123 Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro Ser Ala Tyr Arg Phe Gly
124 65          70          75          80
127 Arg Leu Ser His His Ser Phe Phe Ser Arg His His Pro Gln Pro Gln
128          85          90          95
131 Arg Val Thr His Ile Gln Asp Ile Ala Gly Lys Pro Val Cys Val Val
132          100          105          110
135 Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr Gln Pro Thr Phe Leu Ser
136          115          120          125
139 Arg Cys Leu Met Gly Met Pro Thr Ile Ser Val Pro Ile Gly Asp Pro
140          130          135          140
143 Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr Ser Asp Thr Trp Arg Lys
144 145          150          155          160

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147 Lys Leu Lys Asp Leu Ala Ser Arg Val Thr Val Phe Thr Lys Glu Ile
148           165           170           175
151 Gln Pro Lys Pro Asp Glu Val Gly Val Ala Gln Arg Met Glu Pro Arg
152           180           185           190
155 Lys Lys Arg Pro Ser
156           195
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 1035
161 <212> TYPE: DNA
162 <213> ORGANISM: Mus musculus
165 <220> FEATURE:
166 <221> NAME/KEY: CDS
167 <222> LOCATION: (84)..(779)
168 <223> OTHER INFORMATION: Coding sequence
170 <400> SEQUENCE: 3
171 tcttgagggtt gccaatTTTT tttttttttt tttttttttt tttttttttt ggtttgggga      60
173 gaaacttggtg ttggaaccag ccc ctg ttt ctg ggg aat gta tat aag ggg agt      113
174           Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser
175           1           5           10
177 tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag      161
178 Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
179           15           20           25
181 cca gag acg aag ccg gag aac ctt cca agg agc cac ggg gat gtt ggg      209
182 Pro Glu Thr Lys Pro Glu Asn Leu Pro Arg Ser His Gly Asp Val Gly
183           30           35           40
185 ctc cag aaa gag act gtg gtc cca ggc att gtg gat ttc gag ctg atc      257
186 Leu Gln Lys Glu Thr Val Val Pro Gly Ile Val Asp Phe Glu Leu Ile
187           45           50           55
189 cat gag gag ctg aag acc aca aag ccc caa aca tca caa cca aca ccc      305
190 His Glu Glu Leu Lys Thr Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro
191           60           65           70
193 agt gcc tac cgc ttt gga cgc cta agc cac cat tcc ttc ttc tcg agg      353
194 Ser Ala Tyr Arg Phe Gly Arg Leu Ser His His Ser Phe Phe Ser Arg
195 75           80           85           90
197 cac cac ccc caa cca cag cga gtg act cat atc caa gtt aca gga aga      401
198 His His Pro Gln Pro Gln Arg Val Thr His Ile Gln Val Thr Gly Arg
199           95           100           105
201 gag gac ctg gag cac tcc ctg ccc ctc acc acc tct ttc cag ctc ctt      449
202 Glu Asp Leu Glu His Ser Leu Pro Leu Thr Thr Ser Phe Gln Leu Leu
203           110           115           120
205 caa gct cct ggg gtc cag ccc atg gat ctc act ccc tct gca gat atc      497
206 Gln Ala Pro Gly Val Gln Pro Met Asp Leu Thr Pro Ser Ala Asp Ile
207           125           130           135
209 gct ggg aag cct gtc tgc gtg gtc agg gac gag ttc tct ctg tcg gcc      545
210 Ala Gly Lys Pro Val Cys Val Val Arg Asp Glu Phe Ser Leu Ser Ala
211           140           145           150
213 ttg act cag ccc aca ttc tta tcc cgc tgt ctg atg ggg atg ccc acc      593
214 Leu Thr Gln Pro Thr Phe Leu Ser Arg Cys Leu Met Gly Met Pro Thr
215 155           160           165           170

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217 atc tct gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt      641
218 ile ser val pro ile gly asp pro gln ser asn arg asn pro gln leu
219          175          180          185
221 tct act tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga      689
222 ser thr ser asp thr trp arg lys lys leu lys asp leu ala ser arg
223          190          195          200
225 gtg act gtc ttc act aag gaa atc cag cca aag ccc gat gag gtt ggt      737
226 val thr val phe thr lys glu ile gln pro lys pro asp glu val gly
227          205          210          215
229 gtt gca caa aga atg gag cct aga aaa aaa agg cct tct taa      779
230 val ala gln arg met glu pro arg lys lys arg pro ser
231          220          225          230
233 gtctccccaa tgctcagctg ctggcacggg aggggaagga cctcataac ctggaaggtg      839
235 acagcgaaaaa tcaaagaaac acaaaatcac acctagcaga gaaatccaag aagggttccc      899
237 agaaacacccc tctaaagcaa ctgttcccaa cctgtctaata gccttgaccc ttgaatacag      959
239 tttctcacac tgcagtaacc cctgcccccg aaataaaatt attttcatta ctacttcaaa    1019
241 aaaaaaaaaa aaaaaa      1035
244 <210> SEQ ID NO: 4
245 <211> LENGTH: 231
246 <212> TYPE: PRT
247 <213> ORGANISM: Mus musculus
249 <400> SEQUENCE: 4
251 leu phe leu gly asn val tyr lys gly ser leu ala pro arg arg asp
252 1          5          10          15
255 glu val thr ser pro lys ala glu pro gln pro glu thr lys pro glu
256          20          25          30
259 asn leu pro arg ser his gly asp val gly leu gln lys glu thr val
260          35          40          45
263 val pro gly ile val asp phe glu leu ile his glu glu leu lys thr
264          50          55          60
267 thr lys pro gln thr ser gln pro thr pro ser ala tyr arg phe gly
268 65          70          75          80
271 arg leu ser his his ser phe phe ser arg his his pro gln pro gln
272          85          90          95
275 arg val thr his ile gln val thr gly arg glu asp leu glu his ser
276          100          105          110
279 leu pro leu thr thr ser phe gln leu leu gln ala pro gly val gln
280          115          120          125
283 pro met asp leu thr pro ser ala asp ile ala gly lys pro val cys
284          130          135          140
287 val val arg asp glu phe ser leu ser ala leu thr gln pro thr phe
288 145          150          155          160
291 leu ser arg cys leu met gly met pro thr ile ser val pro ile gly
292          165          170          175
295 asp pro gln ser asn arg asn pro gln leu ser thr ser asp thr trp
296          180          185          190
299 arg lys lys leu lys asp leu ala ser arg val thr val phe thr lys
300          195          200          205
303 glu ile gln pro lys pro asp glu val gly val ala gln arg met glu

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304      210      215      220
307 Pro Arg Lys Lys Arg Pro Ser
308 225      230
311 <210> SEQ ID NO: 5
312 <211> LENGTH: 2117
313 <212> TYPE: DNA
314 <213> ORGANISM: Mus musculus
317 <220> FEATURE:
318 <221> NAME/KEY: CDS
319 <222> LOCATION: (40)..(1365)
321 <220> FEATURE:
322 <221> NAME/KEY: variation
323 <222> LOCATION: (336)..(336)
324 <223> OTHER INFORMATION: results in encoded 'Xaa' at location 99 stands for Val.
326 <220> FEATURE:
327 <221> NAME/KEY: variation
328 <222> LOCATION: (402)..(402)
329 <223> OTHER INFORMATION: results in encoded 'Xaa' at location 121 stands for Val.
331 <220> FEATURE:
332 <221> NAME/KEY: variation
333 <222> LOCATION: (420)..(420)
334 <223> OTHER INFORMATION: results in encoded 'Xaa' at location 127 stands for Ile.
336 <220> FEATURE:
337 <221> NAME/KEY: variation
338 <222> LOCATION: (705)..(705)
339 <223> OTHER INFORMATION: results in encoded 'Xaa' at location 222 stands for Pro.
341 <400> SEQUENCE: 5
342 aagaaaagaa ggagaataga ggagctgctg gctgagaaa atg gct gtt gat ggt      54
343                               Met Ala Val Asp Gly
344                               1           5
346 ggg tgt ggg gac act gga gac tgg gaa ggt cgc tgg aac cat gta aag      102
347 Gly Cys Gly Asp Thr Gly Asp Trp Glu Gly Arg Trp Asn His Val Lys
348           10           15           20
350 aag ttc ctc gag cgg tct gga ccc ttc aca cac ccc gat ttc gaa cca      150
351 Lys Phe Leu Glu Arg Ser Gly Pro Phe Thr His Pro Asp Phe Glu Pro
352           25           30           35
354 agc act gaa tca ctc cag ttc ttg tta gat aca tgt aaa gtt cta gtc      198
355 Ser Thr Glu Ser Leu Gln Phe Leu Leu Asp Thr Cys Lys Val Leu Val
356           40           45           50
358 att gga gct ggt ggc tta gga tgt gag ctt ctg aaa aat ctg gca tta      246
359 Ile Gly Ala Gly Gly Leu Gly Cys Glu Leu Leu Lys Asn Leu Ala Leu
360           55           60           65
362 tct ggt ttt aga cag att cat gtt ata gac atg gac act ata gat gtt      294
363 Ser Gly Phe Arg Gln Ile His Val Ile Asp Met Asp Thr Ile Asp Val
364 70           75           80           85
366 tcc aat tta aat aga cag ttt tta ttt agg cct aaa gat gty gga aga      342
W--> 367 Ser Asn Leu Asn Arg Gln Phe Leu Phe Arg Pro Lys Asp Xaa Gly Arg
368           90           95           100
370 ccc aag gct gaa gtt gct gca gaa ttc cta aat gac aga gtt cct aac      390

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/579,879A

DATE: 03/06/2007
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Input Set : N:\efs\03_06_07

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 99,121,127,222 ✓

Seq#:6; Xaa Pos. 99,121,127,222 ✓

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:342
M:341 Repeated in SeqNo=5
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:96
M:341 Repeated in SeqNo=6